IN THE CLAIMS

This listing of claims will replace all prior versions, and listings, of the claims in the application.

1.   *(Canceled)*

2.   *(Canceled)*

3.   *(Previously amended)* A method in a computer system for displaying data on gene expression in a molecular topography, comprising:

(a)   generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i)   a first value for a first polynucleotide characteristic comprising a sequence identifier;

(ii)   a second value for a second polynucleotide-characteristic different from said first characteristic comprising a measure of size of the polynucleotide; and

(iii)   a third value that is a measure of the quantity of the polynucleotide;

(b)   calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

(c)   displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression.

4.   *(Canceled)*

5.   *(Canceled)*

6.   *(Canceled)*

7.   *(Canceled)*

8.   *(Canceled)*

9.   *(Canceled)*

10.   *(Canceled)*

11.   (*Previously amended*) A method in a computer system for displaying differences in gene expression, comprising:

(1)   for each of a first gene expression profile and a second gene expression profile to be compared, generating a molecular topography according to a method in a computer system for analyzing and displaying data on gene expression in a molecular topography, comprising:

(a)   generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i)   a first value for a first polynucleotide characteristic,

(ii)   a second value for a second polynucleotide-characteristic different from said first characteristic, and

(iii)   a third value that is a measure of the quantity of the polynucleotide;

(b)   calculating for each polynucleotide from the first and second values a position in a two co-ordinate display space, and from the third value a peak at that position; and

(c)   displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression,

(2)   for each position in the two co-ordinate display space subtracting the measure of quantity in the first gene expression profile from the measure of quantity in the second gene expression profile;

(3)   for each position, generating a peak for display from the difference; and

(4)   displaying the respective difference peak at each of the positions in the two co-ordinate display space.

12.   (*Previously amended*) A method in a computer system for displaying differences in gene expression, comprising:

(1)   for each of a first gene expression profile and a second gene expression profile to

be compared, generating a molecular topography according to a method, comprising:

      (a)   generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

            (i)   a first value for a first polynucleotide characteristic;

            (ii)   a second value for a second polynucleotide-characteristic different from said first characteristic; and

            (iii)   a third value that is a measure of the quantity of the polynucleotide;

      (b)   calculating for each polynucleotide from the first and second values a position in a two-co-ordinate display space, and from the third value calculating a peak at that position; and

      (c)   displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression

      (2)   for each position in the two co-ordinate display space subtracting the measure of quantity in the first gene expression profile from the measure of quantity in the second gene expression profile;

      (3)   for each position, generating a peak for display from the difference; and

      (4)   displaying the respective difference peak at each of the positions in the two co-ordinate display space,

      wherein differences are displayed only if they meet or exceed a threshold value.

      13.   (*Previously amended*) A method in a computer system for comparing gene expression, comprising:

      (1)   for each of a first gene expression profile and a second gene expression profile to be compared, generating a molecular topography according to claim 11,

      (2)   for each position in the two co-ordinate display space subtracting a first measure of quantity in the first profile from a second measure of quantity in the second profile to generate respective difference values;

(3)   calculating from the respective difference values a measure of difference of the two profiles.

14. (*Previously amended*) The method of claim 13, wherein the first profile is a standard reference profile and the second profile is a profile of a test sample.

15. (*Original*) The method of claim 14, wherein comparison of the test sample profile with the standard reference profile is diagnostic of a condition or disease.

16. (*Original*) The method of claim 15, wherein the first profile is a profile of a reference sample and the second profile is a profile of a test sample.

17. (*Original*) The method of claim 16, wherein comparison of the profile of the test sample with the profile of the reference sample is diagnostic of a condition or disease.

18. (*Original*) The method of claim 13 wherein the difference value is set to zero when the difference between the first measure and the second measure is less than two-fold.

19. (*Original*) The method of claim 13 wherein the first profile is identical to the second profile when all the respective first and second measures are identical.

20. (*Original*) The method of claim 13 wherein the first profile is similar to the second profile when the average difference between the respective first and second measures is less than a predefined amount.

21.   (*Canceled*)

22.   (*Canceled*)

23.   (*Canceled*

24.   (*Canceled*)